FIGURE 1-1


```
          -80                 -60                 -40
           .                   .                   .                   .
-28  AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA   31

          -20                 -1                  20
           .                   .                   .                   .
 32  GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC   91
 -8                                 M  N  T  S  H  L  L  A  L  L  L    11

          40                  60                  80
           .                   .                   .                   .
 92  CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT   151
 12  P  K  S  P  Q  G  E  N  R  S  K  P  L  G  T  P  Y  N  F  S    31

         100                 120                 140
           .                   .                   .                   .
152  GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG   211
 32  E  H  C  Q  D  S  V  D  V  M  V  F  I  V  T  S  Y  S  I  E    51

         160                 180                 200
           .                   .                   .                   .
212  ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG   271
 52  T  V  V  G  V  L  G  N  L  C  L  M  C  V  T  V  R  Q  K  E    71
```

FIGURE 1-2

```
        220                 240                 260
         .                   .                   .                   .
272  AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC  331
 72  K  A  N  V  T  N  L  L  I  A  N  L  A  F  S  D  F  L  M  C   91

        280                 300                 320
         .                   .                   .                   .
332  CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG  391
 92  L  L  C  Q  P  L  T  A  V  Y  T  I  M  D  Y  W  I  F  G  E   111

        340                 360                 380
         .                   .                   .                   .
392  ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG  451
112  T  L  C  K  M  S  A  F  I  Q  C  M  S  V  T  V  S  I  L  S   131

        400                 420                 440
         .                   .                   .                   .
452  CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC  511
132  L  V  L  V  A  L  E  R  H  Q  L  I  I  N  P  T  G  W  K  P   151

        460                 480                 500
         .                   .                   .                   .
512  AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC  571
152  S  I  S  Q  A  Y  L  G  I  V  L  I  W  V  I  A  C  V  L  S   171
```

FIGURE 1-3

```
          520                 540                 560
           .                   .                   .                   .                   .                   .
572   CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT   631
172   L  P  F  L  A  N  S  I  L  E  N  V  F  H  K  N  H  S  K  A     191

          580                 600                 620
           .                   .                   .                   .                   .                   .
632   CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC   691
192   L  E  F  L  A  D  K  V  V  C  T  E  S  W  P  L  A  H  H  R     211

          640                 660                 680
           .                   .                   .                   .                   .                   .
692   ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG   751
212   T  I  Y  T  T  F  L  L  L  F  Q  Y  C  L  P  L  G  F  I  L     231

          700                 720                 740
           .                   .                   .                   .                   .                   .
752   GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC   811
232   V  C  Y  A  R  I  Y  R  R  L  Q  R  Q  G  R  V  F  H  K  G     251

          760                 780                 800
           .                   .                   .                   .                   .                   .
812   ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG   871
252   T  Y  S  L  R  A  G  H  M  K  Q  V  N  V  V  L  V  V  M  V     271
```

FIGURE 1-4

```
          820                 840                 860
872  GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC  931
272  V  A  F  A  V  L  W  L  P  L  H  V  F  N  S  L  E  D  W  H   291

          880                 900                 920
932  CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC  991
292  H  E  A  I  P  I  C  H  G  N  L  I  F  L  V  C  H  L  L  A   311

          940                 960                 980
992  ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG  1051
312  M  A  S  T  C  V  N  P  F  I  Y  G  F  L  N  T  N  F  K  K   331

          1000                1020                1040
1052 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT  1111
332  E  I  K  A  L  V  L  T  C  Q  Q  S  A  P  L  E  E  S  E  H   351

          1060                1080                1100
1112 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG  1171
352  L  P  L  S  T  V  H  T  E  V  S  K  G  S  L  R  L  S  G  R   371
```

FIGURE 1-5

```
                1120                 1140                 1160
1172  TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC  1231
372   S  N  P  I  *                                                  375
                1180                 1200                 1220
1232  CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG  1291
```

FIGURE 2-1
FIGURE 2-2
FIGURE 2-3

FIGURE 2-1

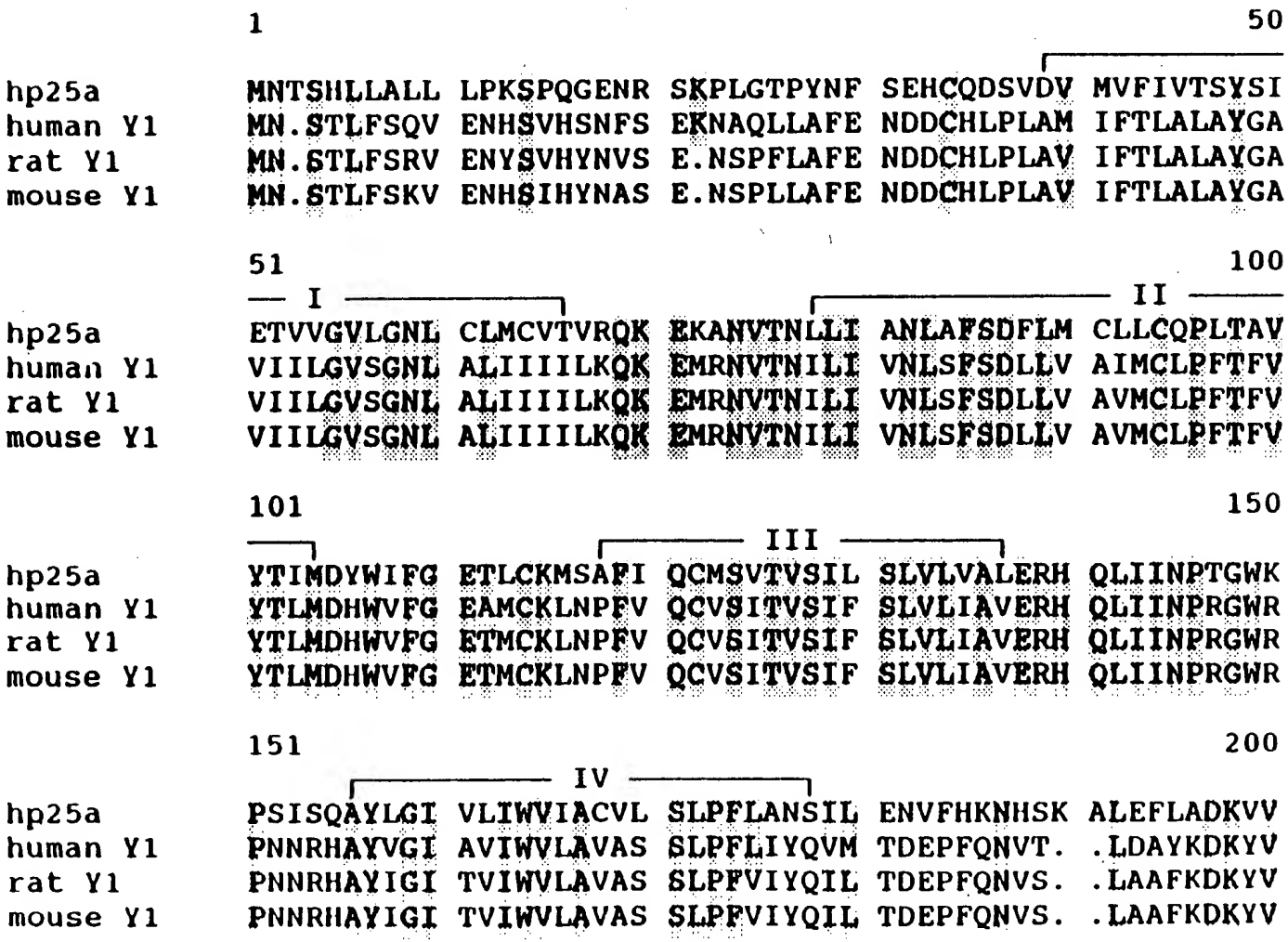


FIGURE 2-2

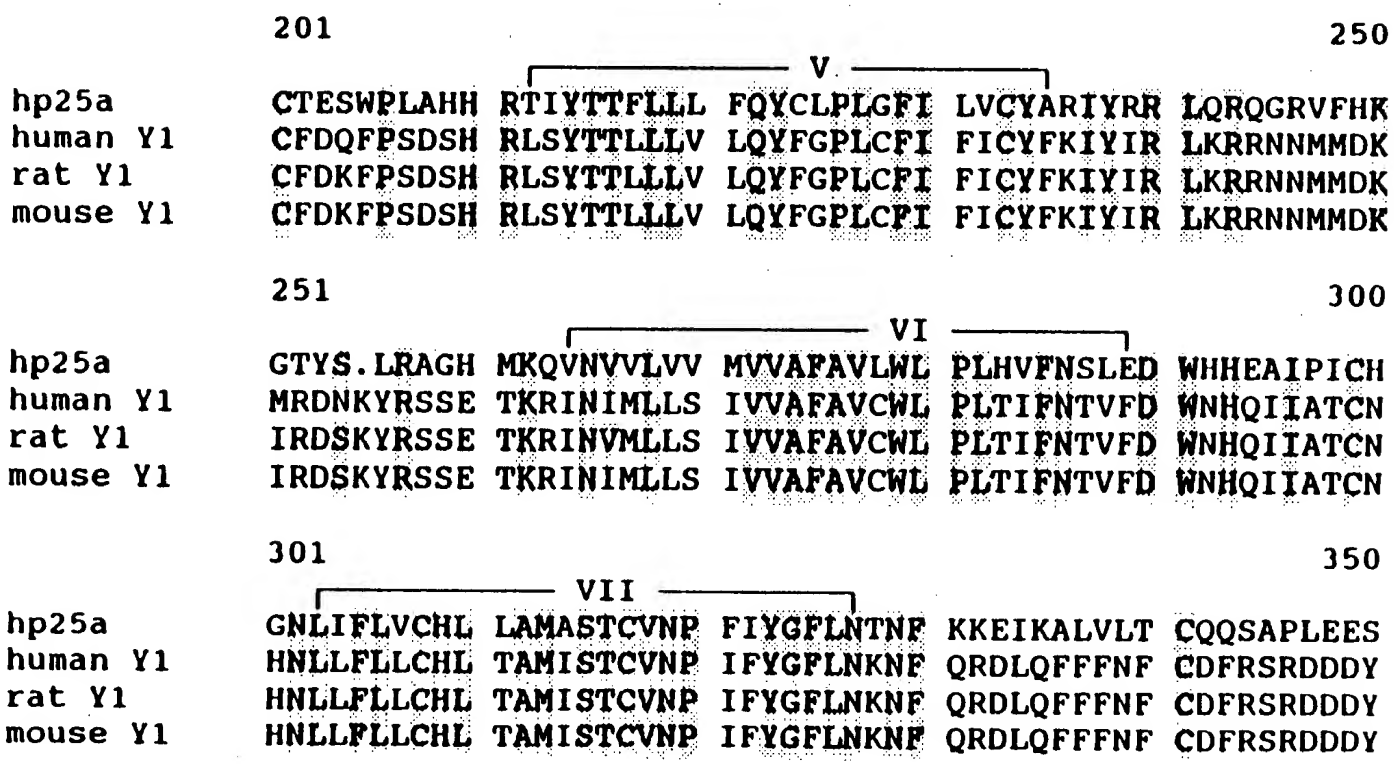

201
250
V
hp25a CTESWPLAHH RTIYTTFLLL FQYCLPLGFI LVCYARIYRR LQRQGRVFHK
human Y1 CFDQFPSDSH RLSYTTLLLV LQYFGPLCFI FICYFKIYIR LKRRNNMMDK
rat Y1 CFDKFPSDSH RLSYTTLLLV LQYFGPLCFI FICYFKIYIR LKRRNNMMDK
mouse Y1 CFDKFPSDSH RLSYTTLLLV LQYFGPLCFI FICYFKIYIR LKRRNNMMDK
251
300
VI
hp25a GTYS.LRAGH MKQVNVVLVV MVVAFAVLWL PLHVFNSLED WHHEAIPICH
human Y1 MRDNKYRSSE TKRINIMLLS IVVAFAVCWL PLTIFNTVFD WNHQIIATCN
rat Y1 IRDSKYRSSE TKRINVMLLS IVVAFAVCWL PLTIFNTVFD WNHQIIATCN
mouse Y1 IRDSKYRSSE TKRINIMLLS IVVAFAVCWL PLTIFNTVFD WNHQIIATCN
301
350
VII
hp25a GNLIFLVCHL LAMASTCVNP FIYGFLNTNF KKEIKALVLT CQQSAPLEES
human Y1 HNLLFLLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFFNF CDFRSRDDDY
rat Y1 HNLLFLLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFFNF CDFRSRDDDY
mouse Y1 HNLLFLLCHL TAMISTCVNP IFYGFLNKNF QRDLQFFFNF CDFRSRDDDY

FIGURE 2-3

```
                351                                     388
hp25a           EHLPLSTVHT EVSKGSLRLS GRSNPI*... ........
human Y1        ETIAMSTMHT DVSKTSLKQA SPVAFKKINN NDDNEKI*
rat Y1          ETIAMSTMHT DVSKTSLKQA SPVAFKKISM N.DNEKI*
mouse Y1        ETIAMSTMHT DVSKTSLKQA SPVAFKKISM N.DNEKV*
```

FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

```
-170                -150                -130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110                -90                 -70

TTCTTACCTGGTTCCATTTTACATGCCTGGACCTTTGAGTTCCATTTGTTTGTTTTGCAG

-50                 -30                 -10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG
                                                              M

10                  30                  50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCCTACAAGGTAAGAATGGGACC
N  T  S  H  L  M  A  S  L  S  P  A  F  L  Q  G  K  N  G  T

70                  90                  110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCGGCAGATCTGTTG
N  P  L  D  S  L  Y  N  L  S  D  G  C  Q  D  S  A  D  L  L

130                 150                 170

GCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGGGGTCCTAGGAAACCTCTGC
A  F  I  I  T  T  Y  S  V  E  T  V  L  G  V  L  G  N  L  C

190                 210                 230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC
L  I  F  V  T  T  R  Q  K  E  K  S  N  V  T  N  L  L  I  A
```

FIGURE 3-2

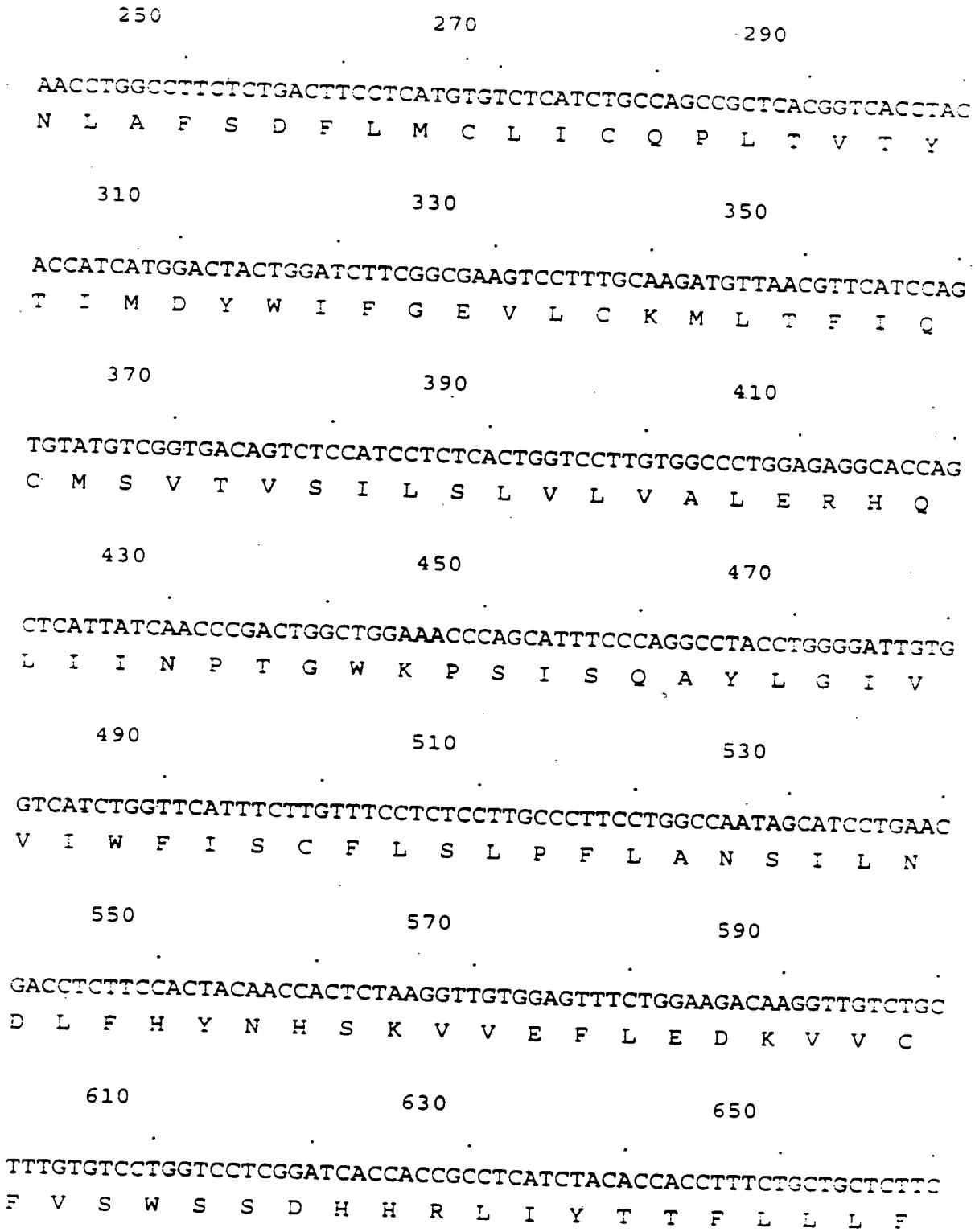

250
270
290
AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC
N L A F S D F L M C L I C Q P L T V T Y
310
330
350
ACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAAGATGTTAACGTTCATCCAG
T I M D Y W I F G E V L C K M L T F I Q
370
390
410
TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCTGGAGAGGCACCAG
C M S V T V S I L S L V L V A L E R H Q
430
450
470
CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCAGGCCTACCTGGGGATTGTG
L I I N P T G W K P S I S Q A Y L G I V
490
510
530
GTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCTGGCCAATAGCATCCTGAAC
V I W F I S C F L S L P F L A N S I L N
550
570
590
GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCTGGAAGACAAGGTTGTCTGC
D L F H Y N H S K V V E F L E D K V V C
610
630
650
TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC
F V S W S S D H H R L I Y T T F L L L F

FIGURE 3-3

```
      670                 690                 710
CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG
Q  Y  C  V  P  L  A  F  I  L  V  C  Y  M  R  I  Y  Q  R  L

      730                 750                 770
CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG
Q  R  Q  R  R  A  F  H  T  H  T  C  S  S  R  V  G  Q  M  K

      790                 810                 830
CGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGCAGTTCTCTGGCTGCCCCTG
R  I  N  G  M  L  M  A  M  V  T  A  F  A  V  L  W  L  P  L

      850                 870                 890
CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC
H  V  F  N  T  L  E  D  W  Y  Q  E  A  I  P  A  C  H  G  N

      910                 930                 950
CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTCATC
L  I  F  L  M  C  H  L  F  A  M  A  S  T  C  V  N  P  F  I

      970                 990                1010
TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT
Y  G  F  L  N  I  N  F  K  K  D  I  K  A  L  V  L  T  C  R

     1030                1050                1070
TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC
C  R  P  P  Q  G  E  P  E  P  L  P  L  S  T  V  H  T  D  L
```

FIGURE 3-4

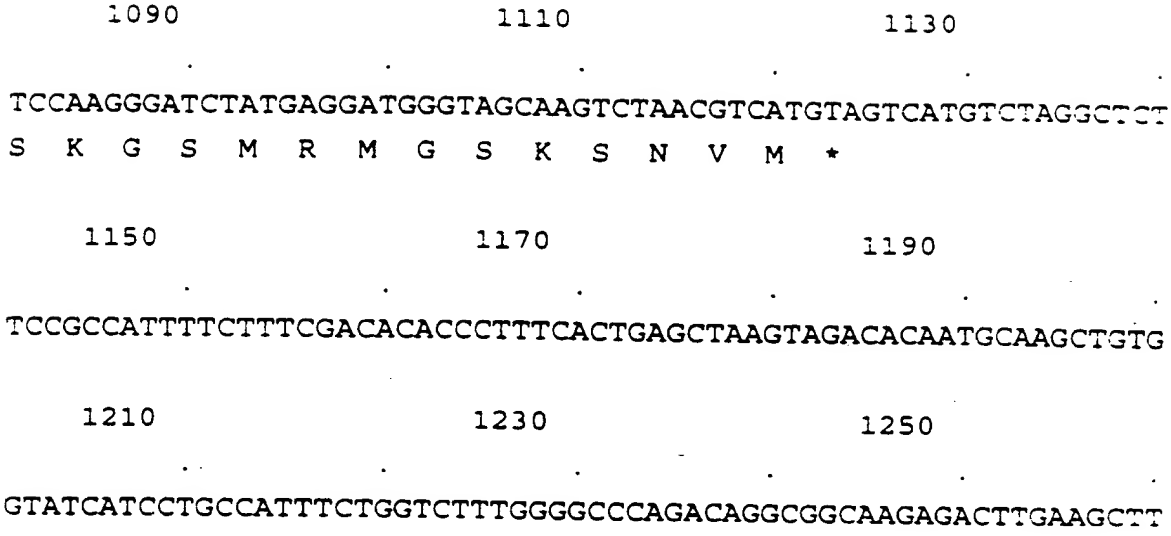

1090
1110
1130
TCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCATGTAGTCATGTCTAGGCTCT
S K G S M R M G S K S N V M *
1150
1170
1190
TCCGCCATTTTCTTTCGACACACCCTTTCACTGAGCTAAGTAGACACAATGCAAGCTGTG
1210
1230
1250
GTATCATCCTGCCATTTCTGGTCTTTGGGGCCCAGACAGGCGGCAAGAGACTTGAAGCTT

FIGURE 4

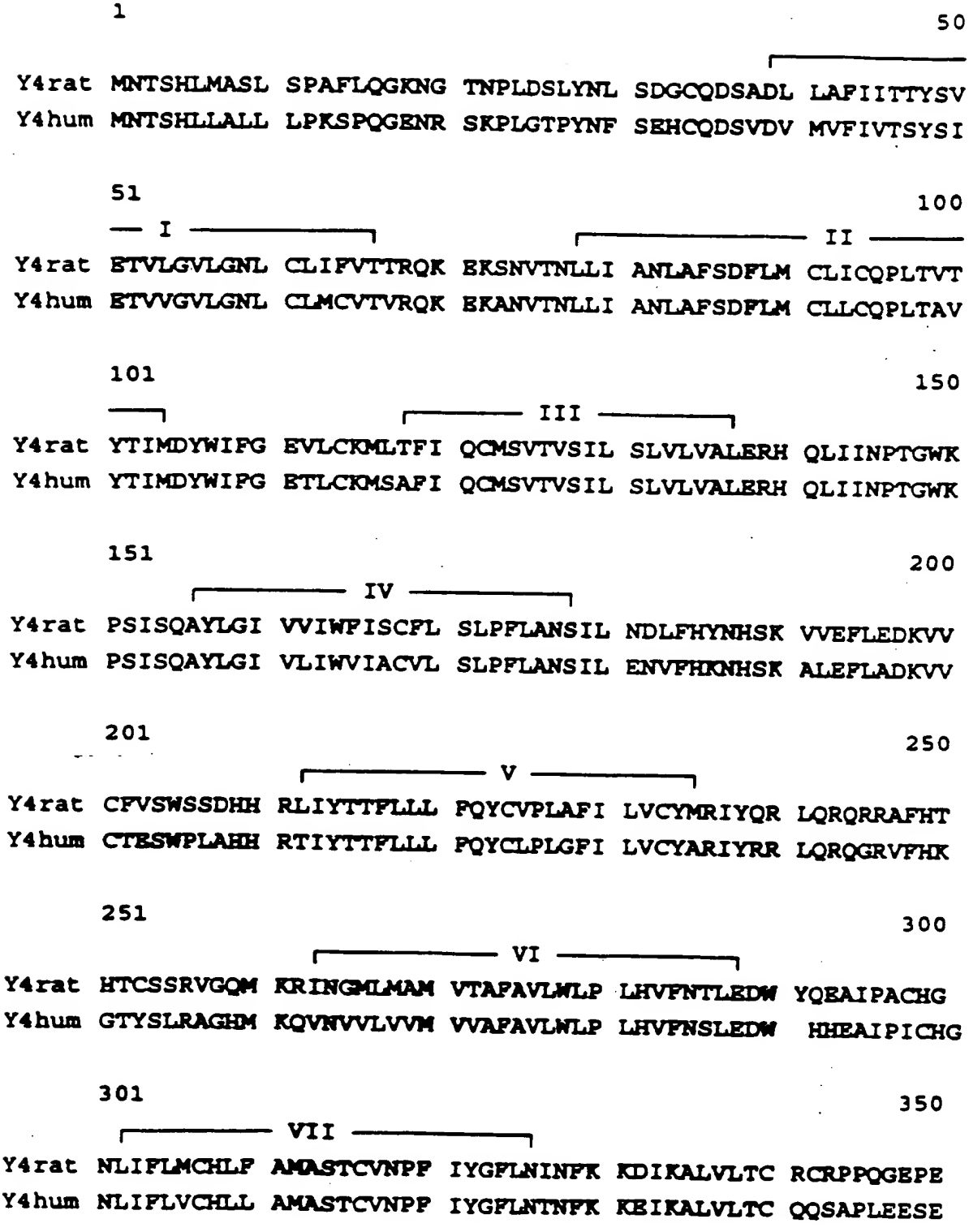

1
50
Y4rat MNTSHLMASL SPAFLQGKNG TNPLDSLYNL SDGCQDSADL LAFIITTYSV
Y4hum MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI
51
100
I
II
Y4rat ETVLGVLGNL CLIFVTTRQK EKSNVTNLLI ANLAFSDFLM CLICQPLTVT
Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLLCQPLTAV
101
150
III
Y4rat YTIMDYWIFG EVLCKMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK
Y4hum YTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK
151
200
IV
Y4rat PSISQAYLGI VVIWFISCFL SLPFLANSIL NDLFHYNHSK VVEFLEDKVV
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKNHSK ALEFLADKVV
201
250
V
Y4rat CFVSWSSDHH RLIYTTFLLL FQYCVPLAFI LVCYMRIYQR LQRQRRAFHT
Y4hum CTESWPLAHH RTIYTTFLLL FQYCLPLGFI LVCYARIYRR LQRQGRVFHK
251
300
VI
Y4rat HTCSSRVGQM KRINGMLMAM VTAFAVLWLP LHVFNTLEDW YQEAIPACHG
Y4hum GTYSLRAGHM KQVNVVLVVM VVAFAVLWLP LHVFNSLEDW HHEAIPICHG
301
350
VII
Y4rat NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTC RCRPPQGEPE
Y4hum NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KEIKALVLTC QQSAPLEESE

FIGURE 5

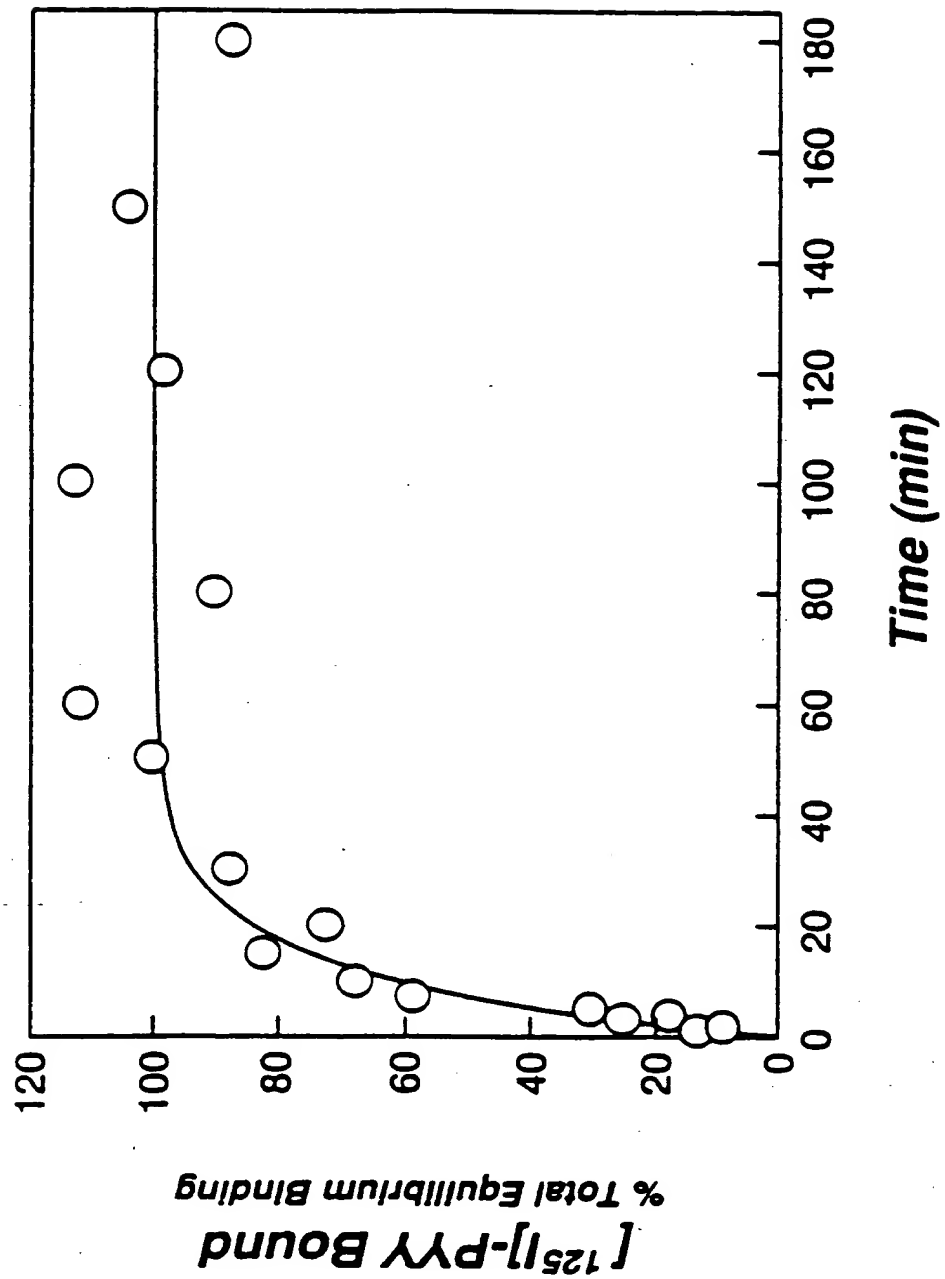
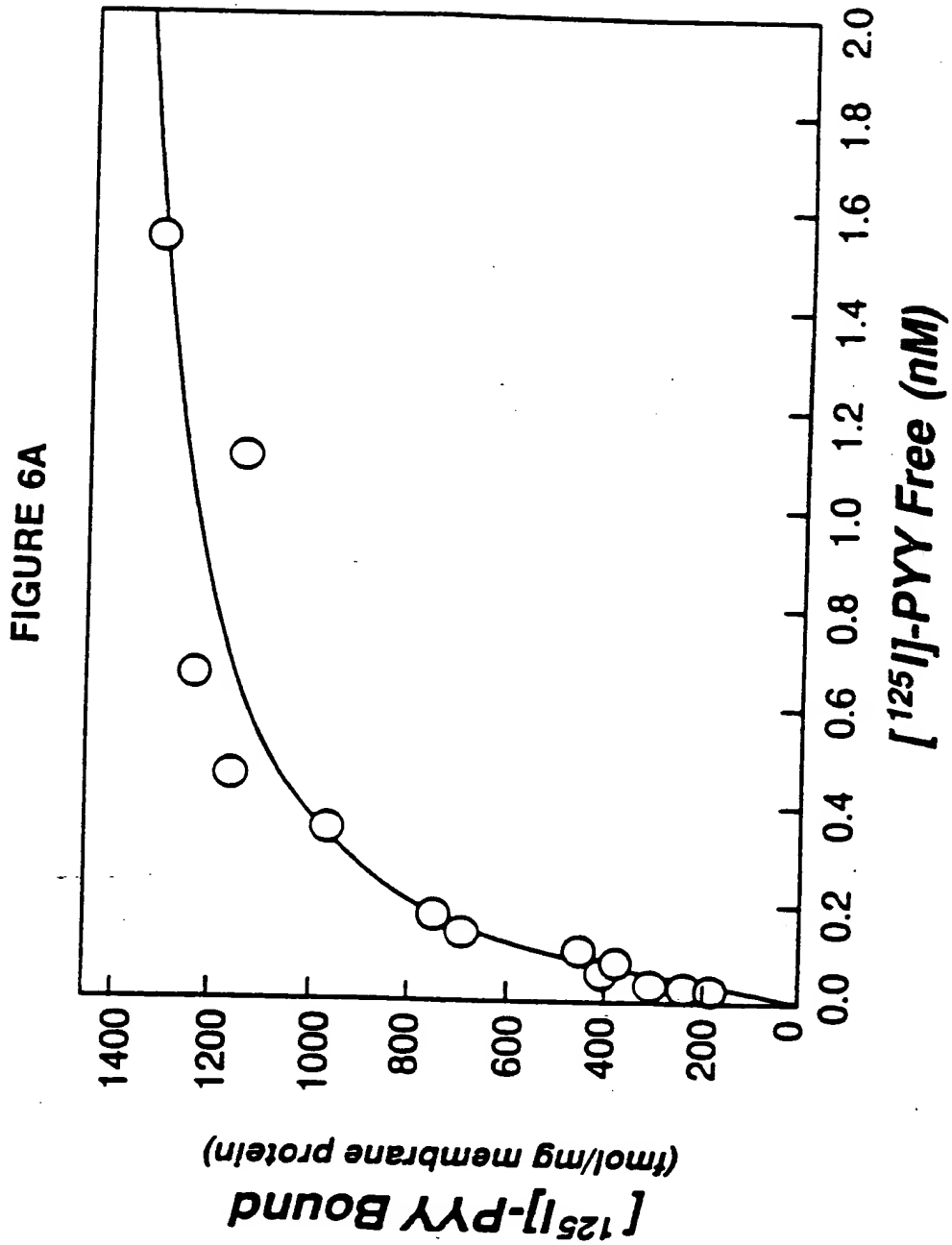

[125I]-PYY Bound
% Total Equilibrium Binding
120
100
80
60
40
20
0
0
20
40
60
80
100
120
140
160
180
Time (min)

FIGURE 6A


[125I]-PYY Bound
(fmol/mg membrane protein)
1400
1200
1000
800
600
400
200
0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
1.8
2.0
[125I]-PYY Free (nM)

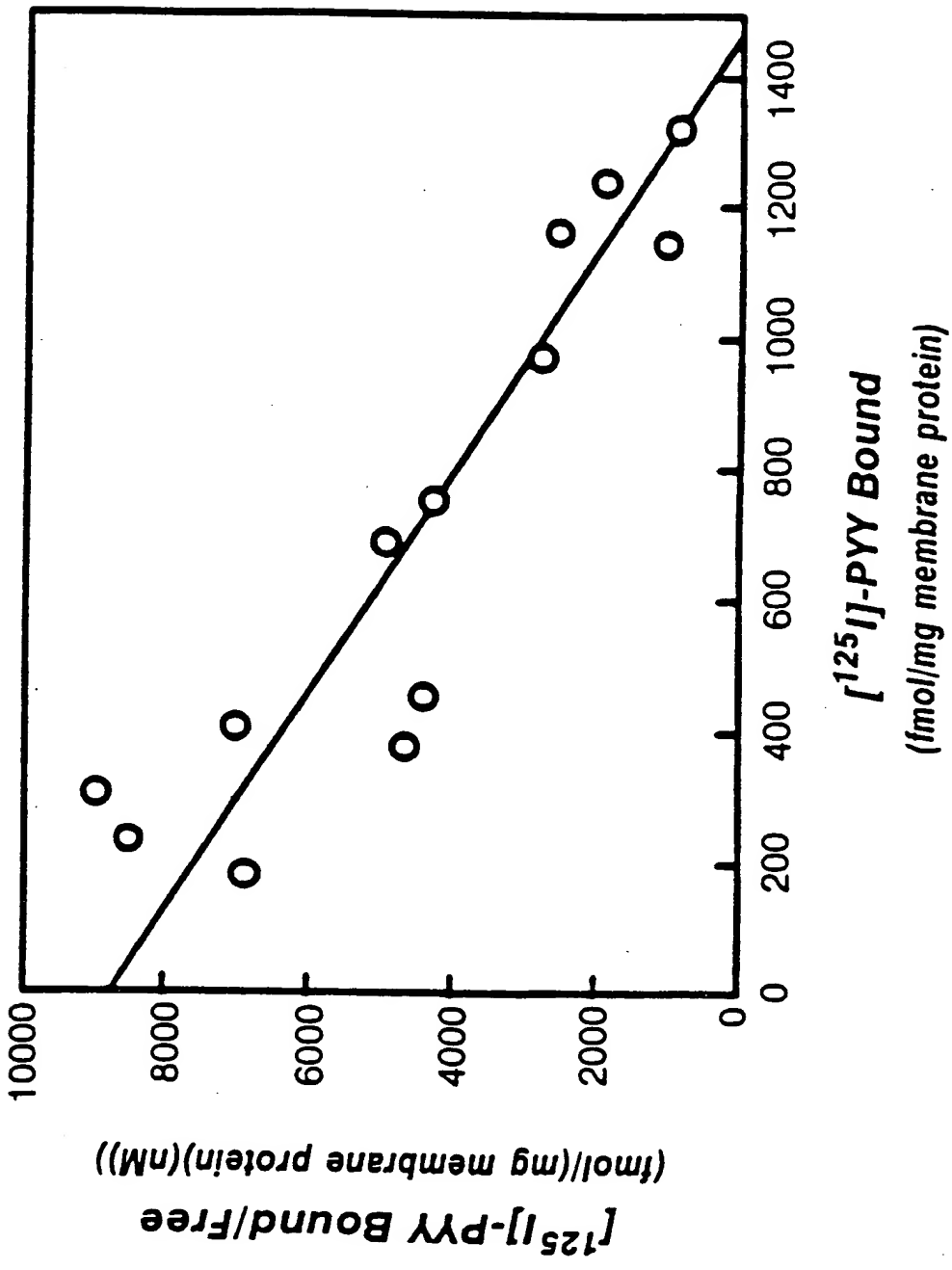

[125I]-PYY Bound/Free
(fmol/(mg membrane protein)(nM))
10000
8000
6000
4000
2000
0
0
200
400
600
800
1000
1200
1400
[125I]-PYY Bound
(fmol/mg membrane protein)

FIGURE 6B

FIGURE 7

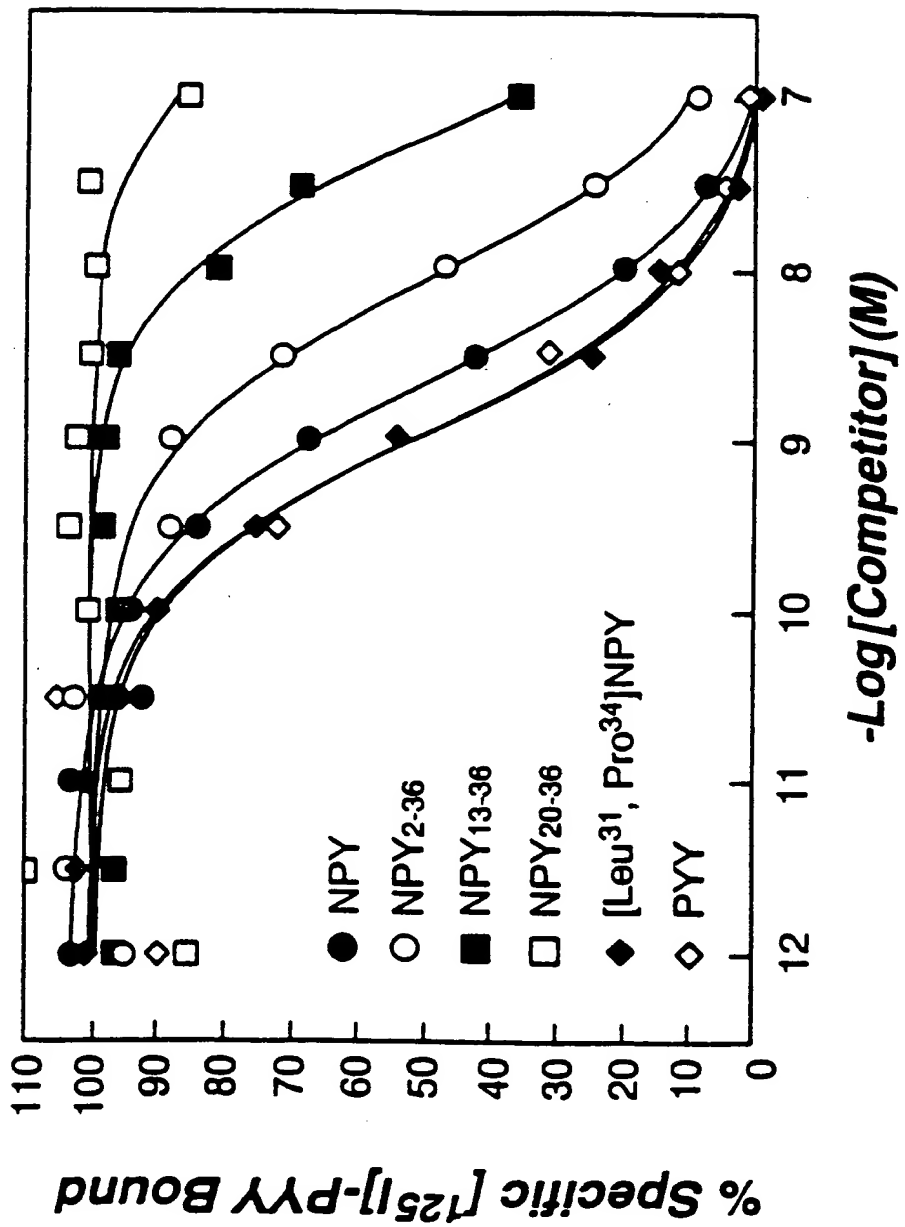

% Specific [125I]-PYY Bound
110
100
90
80
70
60
50
40
30
20
10
0
12
11
10
9
8
7
-Log[Competitor](M)
NPY
NPY2-36
NPY13-36
NPY20-36
[Leu31, Pro34]NPY
PYY

FIGURE 8

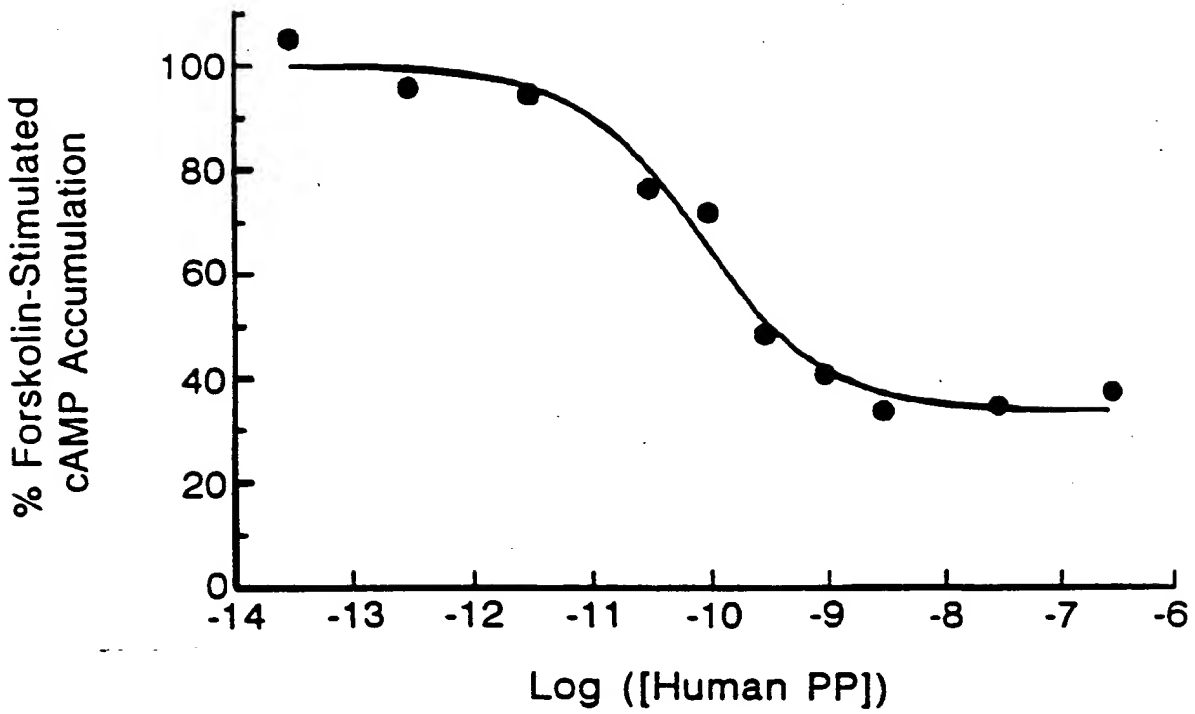

% Forskolin-Stimulated cAMP Accumulation
100
80
60
40
20
0
-14
-13
-12
-11
-10
-9
-8
-7
-6
Log ([Human PP])

FIGURE 9A

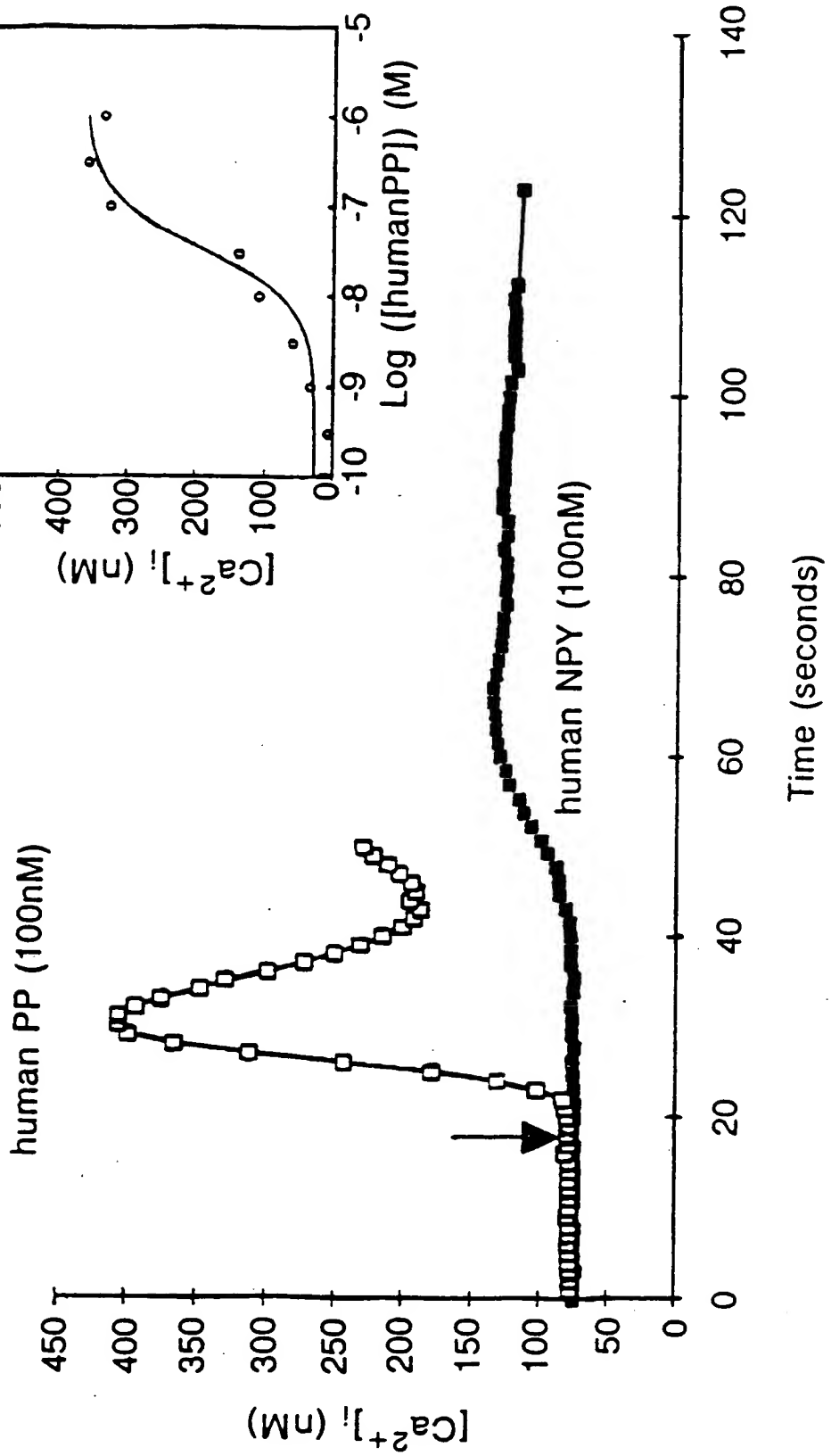


FIGURE 9B